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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|---|---|---|---|
| 09/314,698 | 05/19/1999 | STEVEN PERRIN | 14791-501(AR | 5542 |

7590 08/27/2002

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| ART UNIT | PAPER NUMBER |
|---|---|
| 1634 | |

DATE MAILED: 08/27/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

| Office Action Summary | Application No. 09/314,698 | Applicant(s) PERRIN ET AL. | |
|---|---|---|---|
| | Examiner Juliet C Einsmann | Art Unit 1634 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on *10 June 2002* .

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *27-57* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *27-57* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

**Priority under 35 U.S.C. §§ 119 and 120**

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

**Attachment(s)**

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____ .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

## DETAILED ACTION

### *Continued Examination Under 37 CFR 1.114*

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 6/10/02 has been entered.

2. Claims 1-10 and 12-26 were cancelled and claims 27-57 were added.

3. The drawings remain objected to for the reasons set forth in the PTO-948 mailed with paper number 5. A complete response to this office action will include drawing corrections as required by PTO-948. The filing of drawing corrections cannot be held in abeyance. See 37 CFR 1.85(a).

### *Claim Rejections - 35 USC § 112*

4. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

5. Claims 27-57 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 27, 41, 48, 49, 52, and 55 are indefinite because it is not clear what the phrase "on said microarray" is meant to modify. That is, it is not clear from the structure of the claims if

"on said microarray" is meant to designate that the sequencing reaction occurs on the surface of the microarray, or that the fragment on the microarray is sequenced. It appears from applicant's remarks contained with the amendment (p. 7-12 of paper number 21) that applicant intends for the sequencing reaction to occur on the surface of the microarray, and as such, the claim should be clarified to indicate as much. The newly set forth rejections under 112 1st paragraph address this limitation as if it requires the sequencing reaction to occur on the surface of the microarray, and the art rejections set forth herein address this limitation as if it requires that the fragment on the microarray is sequenced.

Claims 27 and 41 are indefinite because it is not clear how the amplifying step of (d) relates to the sequencing step of (e). Generally, when nucleic acids are amplified, such amplification reactions occur in solution. Thus, it is not clear how following amplification, the "amplified non-redundant nucleic acid fragment" can be sequenced on the surface of the array or that it is a fragment on an array, and so it is not clear what is meant by "on said microarray."

The phrase "the DNA" in claims 29, 30, and 31 lacks proper antecedent basis because these claims do not previously recite "DNA," nor does claim 27 from which these claims depend.

Claim 34 is indefinite over the recitation "without isolating said fragments" because it is not clear what applicant considers to be a step of isolating fragments. Every known type of sequencing reaction requires some level of isolation of the nucleic acid to be sequenced, at least to ensure that it is a homogeneous sample to be sequenced, and thus, it is not clear how the two fragments in step (f) of claim 34 can be sequenced without any isolation step.

The phrase "the DNA" in claims 36, 37, and 38 lacks proper antecedent basis because these claims do not previously recite "DNA," nor does claim 34 from which these claims depend.

Claim 41 is indefinite because it has two steps labeled (f), and then the second step (f) indicates the repetition of step (f). Amendment of the claim to indicate that the final step of the method is step (g) would obviate this rejection.

The phrase "the DNA" in claims 43, 44, and 45 lacks proper antecedent basis because these claims do not previously recite "DNA," nor does claim 41 from which these claims depend.

Regarding claim 55, the phrase "particularly" renders the claim indefinite because it is unclear whether the limitation(s) following the phrase are part of the claimed invention. Furthermore, the term "decreased" in claim 55 is a relative term which renders the claim indefinite. The term "decreased" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention. The claim does not indicate a standard from which the hybridization stringencies are decreased.

The dependent claims are all rejected herein as they contain the same indefinite language as has been described for the independent claims.

6. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 27-57 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

MPEP 2163.06 notes "If new matter is added to the claims, the examiner should reject the claims under 35 U.S.C. 112, first paragraph - written description requirement. In re Rasmussen , 650 F.2d 1212, 211 USPQ 323 (CCPA 1981)."

Further, it is noted that the MPEP teaches,

> "Any negative limitation or exclusionary proviso must have basis in the original disclosure. See Ex parte Grasselli , 231 USPQ 393 (Bd. App. 1983) aff'd mem., 738 F.2d 453 (Fed. Cir. 1984). The mere absence of a positive recitation is not basis for an exclusion. Any claim containing a negative limitation which does not have basis in the original disclosure should be rejected under 35 U.S.C. 112, first paragraph as failing to comply with the written description requirement (MPEP 2173.05(i))."

In claim 27, the amplification step of step (d) appears to represent new matter. Also in claim 27, the new limitation of "sequencing said amplified non-redundant nucleic acid *on said microarray*" appears to represent new matter (emphasis added).

In claim 34, the amplifying of step (e) appears to represent new matter. Also in claim 34, the new negative limitation "without isolating said fragments" in step (f) appears to represent new matter. Specifically, the exclusion proviso "without isolating said fragments" is not found in the specification.

In claim 41, the amplification step of step (e) appears to represent new matter. Also in claim 41, the new limitation of "determining the sequence of the fragment amplified in step (d) *on said microarray*" appears to represent new matter (emphasis added).

In claims 48 and 52, the new limitation of "determining the identity of the DNA fragment by DNA sequencing of the fragment identified in step (d) *on said microarray*" appears to represent new matter (emphasis added).

In claim 49, the new limitation of "sequencing the DNA fragment detected in step (d) *on said microarray*" appears to represent new matter (emphasis added).

In claim 55 the new limitation of "sequencing the one or more DNA fragments detected in step (d) *on said microarray*" appears to represent new matter (emphasis added).

No specific basis for these limitations was identified in the specification, nor did a review of the specification by the examiner find any basis for the limitation. Applicant's remarks filed with the amendment merely asserted "The claims, as amended herein, are fully supported by the instant specification and the claims as originally filed (p. 7 of response)." However, a careful review of the claims as originally filed and the specification did not result in the identification of descriptive support for these new claim limitations.

The specification and the claims as originally filed include steps in which the fragments in the original sample are amplified prior to the hybridization step (see original claim 8, for example), but the specification and claims as originally filed do not discuss the amplification of the non-hybridized or weakly hybridized sequence as claimed in claims 27, 34, and 41.

The specification also does not teach a step in which a sequencing reaction occurs on the surface of the array or without isolating the fragment to be sequenced. On page 11 of the specification, applicant teaches "Clones with a weak signal or no signal at all are sequenced. DNA sequencing methods are well known in the art." The specification then cites a few well

known methods for DNA sequencing. None of these methods involve direct sequencing on a microarray, and the specification does not state that any of these methods are carried out "without isolating said fragments." In Example 3.3, applicant discusses the sequencing of clones that did not hybridize simply by saying they were "targeted for EST (expressed sequence tag) sequencing, using techniques well-known in the art (specification p. 20)." Further, the specification teaches "The nucleic acid fragments isolated and sequence in this step... (p. 11, lines 19-20)" which in itself implies that the nucleic acids are isolated prior to sequencing. Since no basis has been identified for any of these limitations by applicant or by the examiner, the claims are rejected as incorporating new matter.

All of the dependent claims rejected herein are rejected because they depend from one of these specifically mentioned independent claims and thus incorporate the same new matter as the independent claim.

8. Claims 27-57 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

This rejection applies to the instant claims when "on said array" and "without isolating said sequence" is interpreted to indicate that the sequencing reaction itself must occur on the surface of the array, without removing the sequence of interest from the array. This interpretation is based on the claim as written as well as applicant's remarks filed with the

amendment entering these claims which repeatedly refers to a reaction that occurs on the surface of the microarray (see Remarks in paper number 21).

The claims encompass methods in which involve a number of method steps, but essentially each embodiment in the claims contains a step in which a hybridization reaction occurs between nucleic acids immobilized on a microarray and nucleic acids in solution. Subsequent to the hybridization reaction, the claims recite a sequencing step in which a nucleic acid is sequenced on the array. In some cases there is an intermediate amplification reaction.

The specification provides no guidance as to how one should carry out the sequencing reaction on the array. The array itself is a collection of random nucleic acid fragments, and in the method when sequencing occurs, some of the fragments on the array are hybridized and some are single stranded. With regard to sequencing, the specification merely teaches that DNA sequencing methods known in the art are to be used, citing the widely used methods of Maxam/Gilbert and Sanger (see specification page 11). However, neither of these methods are sequencing reactions that occur on the surface of an array, and both of them require some level of isolation of a nucleic acid fragment to ensure that only one fragment's sequence is being determined. In the examples, the specification provides that "Clones which did not hybridize in step 3.1 were targeted for EST (expressed sequence tag) sequencing, using techniques well known in the art. Adams et al. SCIENCE 252 :1651-1656 (1991) (specification, page 20)." Adams et al., cited in the specification, sequences using a cycle sequencing method which utilizes a thermal cycler and does not occur on the surface of the array (see Adams, pages 1652 and 1656).

The prior art is silent as to how to perform sequencing reactions on the surface of an array when the array is a heterogeneous mixture of oligonucleotides. In methods where random arrays are hybridized with probes and then some of the immobilized fragments have their sequences determined, such sequencing is undertaken by isolation of the sequence of interest. For example, Gress et al. teach that the sequences of interest are amplified and then further manipulated (p. 611). Thus, the prior art does not provide any guidance as to how to obtain the instantly claimed method.

It is highly unpredictable how the on surface amplification and sequencing of the instantly claimed invention would occur. The fact that the array is made up of a heterogeneous set of fragments whose sequences are random (as required by the claims) would preclude any sequencing by hybridization methodologies because such methodologies would result in many different signals from the array. Extensive experimentation and discovery would have to occur in order to develop the methodologies necessary for the practice of the claimed invention.

Thus, for all of these reasons, it is concluded that undue experimentation would be necessary to practice the claimed invention.

***Claim Rejections - 35 USC § 102***

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. Claims 48 and 52-57 are rejected under 35 U.S.C. 102(b) as being anticipated by Heller et al. (PNAS USA, Vol. 94, p. 2150-2155, March 1997).

Heller et al. teach a method comprising the following steps:

amplifying a random sample of nucleic acid fragments (p. 2151);

immobilizing the random sample of nucleic acids on a solid surface in a microarray format (p. 2151);

hybridizing labeled probes from a DNA source to the immobilized nucleic acid fragments (p. 2151);

detecting fragments which show absent, significantly lesser, or significantly greater hybridization to a labeled probe relative to fragments from another source (p. 2154);

sequencing the DNA fragment detected in step (d) on said microarray, thereby identifying changes in copy of DNA sequences between different sources (p. 2154).

This reference teaches all of the limitations of the rejected claims when "on said microarray" is interpreted to modify the DNA fragment, thus indicating that the fragment was detected on said microarray, as is the case in the teachings of Heller et al. Heller et al. utilized an array of 1046 randomly selected cDNAs from a peripheral blood cDNA library (p. 2154), and hybridized thereto differentially labeled cDNAs from two sources. Heller et al. sequenced cDNAs that were up-regulated in RA tissue relative to IBD, thus, these sequences were under-represented in the IBD sample and over-represented in the RA sample (p. 2154). Heller et al. repeated the immobilization, hybridization, detection and determining steps in order to test different samples of RA that had been maintained in growth medium for different periods of time

(p. 2154). With regard to claim 55, selected sequences hybridized weakly to the cDNA from the IBD samples relative to the cDNA from the RA. Furthermore, Heller et al. teach a step of comparing DNA sequences obtained to other available DNA sequences to detect sequences which show homology but are not identical to other known sequences (p. 2154).

Thus, Heller et al. meet all of the limitations of the instantly rejected claims.

***Claim Rejections - 35 USC § 103***

11. The following prior art rejections apply when the "on said microarray" language is read to modify the fragment to be sequenced, thus indicating that the fragment to be sequenced is the fragment on said microarray.

12. Claims 49-51 are rejected under 35 U.S.C. 103(a) as being unpatentable over Heller et al. (PNAS Vol. 94, pp. 2150-2155, March 1997).

Heller et al. teach a method comprising the following steps:

amplifying a random sample of nucleic acid fragments (p. 2151);

immobilizing the random sample of nucleic acids on a solid surface in a microarray format (p. 2151);

hybridizing labeled probes from a first source and labeled probes from a second source to the immobilized nucleic acid fragments (p. 2151);

detecting fragments which show absent, significantly lesser, or significantly greater hybridization to a labeled probe relative to fragments from another source (p. 2154);

sequencing the DNA fragment detected in step (d) on said microarray, thereby identifying nucleic acid sources that are present in different amounts in a first source and a second source (p. 2154).

This applies to the rejected claims when "on said microarray" is interpreted to modify the DNA fragment, thus indicating that the fragment was detected on said microarray, as is the case in the teachings of Heller et al. Heller et al. utilized an array of 1046 randomly selected cDNAs from a peripheral blood cDNA library (p. 2154), and hybridized thereto differentially labeled cDNAs from two sources. Heller et al. sequenced cDNAs that were up-regulated in RA tissue relative to IBD, thus, these sequences were under-represented in the IBD sample and over-represented in the RA sample (p. 2154).

Heller et al. do not specifically teach a situation in which a fragment that hybridized to a labeled probe from the first source but which did not hybridize to a labeled probe from a second source. Such a situation is completely dependent upon the samples selected and the random probes on the array, and in a sense is a matter of experimental selection. Heller et al. do specifically teach the detection of fragments are differentially hybridized between one sample and another. Thus, in light of all of these teachings, it would have been prima facie obvious in view of the teachings of Heller et al. to have sequenced a fragment that hybridized to probes from one sample and not to probes from a different sample. The ordinary practitioner would have been motivated to sequence such a fragment in order to identify a gene that is differentially expressed from one sample to another, since Heller et al. teach "This technology could provide

new targets for drug development and disease therapies, and in doing so allow for improved treatment of chronic diseases that are challenging because of their complexity."

13. Claims 27-33, 41-47, and 52-54 are rejected under 35 U.S.C. 103(a) as being unpatentable over Kayne et al. (WO 9843088) in view of Gress *et al.* (Mammalian Genome 3: 609-612, 1992).

Kayne et al. teach a method which comprises the steps of:

providing a random sample containing undefined nucleic acid sequences (p. 2, lines 9-10),

hybridizing one or more labeled probes corresponding to previously known or arrayed or sequenced fragments, the sequence of which fragments is known (p. 2, line 8 and p. 3, line 17-18),

identifying at least one fragment that hybridizes weakly or does not hybridize to the labeled probes (p. 2, lines 10-11),

sequencing the non-hybridized nucleic acid sequences (see abstract and p. 9, lines 9-10).

In the method taught by Kayne et al., the collection of defined nucleic acid sequences is bound to a surface (p.2, line 8), wherein the surface may be an array (p. 5, line 31), and the preferred surface for such and array is glass (p. 6, line 12). The method teaches that the sequences to be hybridized to the array should be labeled to permit detection of the DNA which hybridizes to the immobilized sequences (p. 7, line 16-17).

Kayne et al. teach the library of unknown fragments can include gene or gene fragments, may be a random cDNA library, may be genes from an organ, or may be set of RNAs (p. 6, lines 26-28). With respect to claims 33, and step (a) of claims 41-57, Kayne teach that a library may also contain amplified fragments from genomic libraries (p. 4, line 2).

Kayne et al. do not teach a method in which the random sample of nucleic acid fragments is immobilized on a microarray, and Kayne et al. do not teach a method in which the nucleic acids of interest (i.e. the non-hybridized nucleic acids) are amplified from the array.

Thus, with regard to the first difference, the method of Kayne et al. differs from the claimed method because in the method of Kayne et al. the collection of defined nucleic acid sequences is bound to a surface, and in the claimed method the undefined nucleic acid sequences are bound a microarray. However, methods where undefined nucleic acids are placed on an array for screening were known in the art at the time the invention was made. Gress et al. teach a method for hybridization fingerprinting of high-density cDNA-library arrays with cDNA pools in which a random cDNA library is hybridized to a micorarray with the help of a robotic device (p. 609). Gress et al. teach that the spotting cDNAs libraries (i.e. random fragments) onto a microarray allows for the screening of thousands of clones at one time, and also provides a method which is adaptable for automated analysis. With regard to the second difference, Gress et al. teach methods in which nucleic acids on the array are amplified prior to further analysis (p. 611).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have modified the method of Kayne et al. so as to have spotted the library

of random nucleic acids on the microarray in order to have provided an improved method for isolating and identifying non-redundant nucleic acids. The ordinary practitioner would have been motivated to provide an array with a the random nucleic acid library because Gress et al. state, "As we have shown in our work with genomic libraries, such large-scale projects can most easily be performed with library arrays spotted at high clone density with a robotic device..." (p. 613). Such a method would have provided an alternative to the methods of Kayne et al. for the interrogation of unknown sequences for the identification of non-redundant nucleic acids. Furthermore, it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have amplified the nucleic acids of interest identified by the method taught by Kayne et al. in view of Gress et al. The ordinary practitioner would have been motivated to undertake such an amplification in order to provide more template nucleic acid for further manipulation (i.e. such as sequencing).

With respect to claims 41-47 Kayne in view of Gress do not explicitly teach step (f) of the instantly claimed invention, which comprises repeating the hybridization, detection, and identification of the probes which did not hybridize in order to identify additional sequences. However, this step would also have been obvious to a practitioner of ordinary skill in the art for the reasons that follow. Kayne et al. do teach that in some cases it is desired to repeat some steps in the method to control the size and content of the resulting subtraction library (p. 8, lines 7-9), and they specifically teach that "it is preferred that multiple rounds of hybridization are carried out" (p. 8, line 13). Considering this teaching of Kayne et al., it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to have repeated

any of the steps in the method for the added benefit of increasing the amount of sequences detected. Further, "selection of any order of performing process steps is prima facie obvious in the absence of new or unexpected results" (MPEP 2144.04). In the instant case, applicant is simply choosing to repeat already disclosed steps, and this would have been obvious to one of ordinary skill in the art.

Finally, the examiner notes that these claims have different preambles, but substantially the same method steps, and a preamble is generally not accorded any patentable weight where it merely recites the purpose of a process or the intended use of a structure, and where the body of the claim does not depend on the preamble for completeness but, instead, the process steps or structural limitations are able to stand alone. In the case of these claims, the preamble was only directed to the purpose of the process, the steps could stand alone and did not depend on the preamble for completeness, and therefore, the different preambles were not given strong consideration in analysis of the claims (see MPEP 2111.02).

**Response to applicant's remarks**

Rejections over Kayne *et al.* in view of Gress *et al.*

The fundamental difference between the method of Kayne *et al.* in the instantly claimed method is that in the methods of Kayne *et al.* undefined sequences are in solution and the defined nucleic acid sequences are bound to a solid support. Beyond that difference, the teachings of Kayne *et al.* meet all of the limitations of the instant claims as discussed in the rejections. Gress *et al.* clearly provide the teaching and motivation for changing the method of

Kayne *et al.* so as to anchor the undefined sequences in the method taught by Kayne *et al.* onto a solid support, as Gress *et al.* specifically teach that methods which employ such a step allow for the screening of thousands of clones simultaneously as well as the possibility of automation.

Applicant argues at page eight that Gress *et al.* that there is no motivation or rationale in either of the cited references to immobilize DNA fragments of unknown sequence and contact the immobilized unknowns with a solution of DNAs of known sequence because both the immobilized and soluble DNAs of Gress are of unknown sequence. However, this is a piecemeal analysis, considering solely the teachings of Gress et al. In response to applicant's arguments against the references individually, one cannot show nonobviousness by attacking references individually where the rejections are based on combinations of references. See *In re Keller*, 642 F.2d 413, 208 USPQ 871 (CCPA 1981); *In re Merck & Co.*, 800 F.2d 1091, 231 USPQ 375 (Fed. Cir. 1986). Applicant's arguments focus on the fact that Gress does not discuss DNAs of known sequences, however, this teaching is clearly provided by the teachings of Kayne et al. Applicant argues that the examiner has provided no motivation to alter the teachings of Kayne et al. with regard to the "driver sequence," however this is unpersuasive because motivation is provided in the rejection. Gress et al. clearly teaches the advantages of using arrays of unknown sequences to screen unknown sequences. Kayne et al. provide a method for screening unknown sequences to isolate non-redundant sequences. The combination provided in the rejection cites all of the elements of the claimed invention and a motivation for the modification of the teachings in the prior art to arrive at the instantly claimed invention.

Applicant further sets forth that neither Kayne et al. nor Gress et al. teach a step in which the non-redundant sequence is amplified and sequenced on the surface of the microarray (p. 8 of response). However, the claims do not clearly provide such a limitation (see 112 2nd paragraph rejection). If such limitations were clearly present, the rejection over Kayne et al. in view of Gress et al. would have been withdrawn.

***Conclusion***

14. No claims are allowed.

15. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Juliet C. Einsmann whose telephone number is (703) 306-5824. The examiner can normally be reached on Monday through Thursday, 7:00 AM to 4:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, W. Gary Jones can be reached on (703) 308-1152. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 and (703) 305-3014.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.

Juliet C. Einsmann
Examiner
Art Unit 1655

August 23, 2002

W. Gary Jones
Supervisory Patent Examiner
Technology Center 1600